SEG ID NO 9

aliga no. 1 (length 475), 98%, between 83 and 474 alrgn no. 1 (langth 473), 97%; between 36 and 473 ailgn no. 1 (length 462), 95%, belyneen 39 and 462 a.ign no. 1 (length 201), 99%, between 5 and 301 a.gri no. 1 (fength 390), 100%, between 369 and j align no. 1 (langin 384), 99%, belween 1 and 384 align no. 1 (longth 392), 99%, between 1 and 391 →473 (SEQ ID NO 4) 474 (SEQ ID NO 3) -462 (SEQ ID NO 5) 5 301 (SEQ ID NO 1) →391 (SEQ ID KO 2) 364 (SEQ ID NO 6) 18

FIGI

## BLASTP ALIGNMENT OF SEQ ID NO: 10, STEM CELL GROWTH FACTOR-LIKE POLYPEPTIDE WITH MOUSE ID NO: 25 THROMBOSPONDIN TYPE 1 DOMAIN POLYPEPTIDE SEQ

Query: Stem cell growth factor-like plypeptide (SEQ ID NO: 13) Subjet: dbj|BAA75640.1| (AB016768) thrombospondin type 1 domain (Mus musculus) (SEQ ID NO: 25)

Score = 634 (228.2 bits), Expect = 7.8e-62, P = 7.8e-62 Identities = 112/237 (47%), Positives = 152/237 (64%) 19 IGSQNASRGRRQRRMHPXVSQGCQGGCATCSDYNGCLSCKPRLF?ALERIGMKQIGVCLS 78 Query:

SQ C GC CS+ NGCL C P+LF LER ++Q+GVCL +G+RQRR+

19 VGSRGI-KGKRDRRISABGSQACAKGCELCSBVNGCLKCSPKLFILLERNDIRQVGVCLP 77 Sbjct:

79 SCPSGYYGTRYPDINKCTKCKAD-CDTCFNKYFCTKCKSG?YLHLGKCLDNCPEGLEANN 137 Query:

SCP GY+ R PD+NXC KCK + C+ C7+ NFCTKC+ YJH G+C CPEG A N Sbjct:

78 SCPPGYFDARNPDMNKCIKCKIEHCEACFSHNFCTKCQEALYLHKGRCYPACPEGSTAAN 137

138 HTMECVSIVHCEVSEWNZWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETR 197 Query:

138 STMECGSPAQCEMSEWSPWGPCSKRRLCGFRKGSEERTRRVLHAPGGDHTTCSDTKETR 197 TMBC S CE+SEM+PW PC+KK K CGF++G+E R R ++ P Sbjct:

198 KCTVQRKKCGKGERGKKGRERKAKKPNKGESKEAIPDSKSLESSKEIPEQRANKQQQ 254 KCTV+R C +G++ +KG + +R+ N+ +++ +SK Query:

198 KCTVRRTPCPEGQKRRKGGGGRRZNAMRHPARK---NSKEPRSNS----RAHKGQQQ 247 Sbjct:

## BLASTP ALIGNMENT OF SEQ ID NO: 10, STEM CELL GROWTH FACTOR-LIKE POLYPEPTIDE WITH HUMAN POLYPEPTIDE SEQ ID NO: 26 CLONE DA228\_6 SECRETED PROTEIN

Query: Stem cell growth factor-like plypeptide (SEQ ID NG: 10) Subjet: sp|N85607|W85607 Secreted protein clone da228\_6 (SEQ ID NO: 26) Length = 292

Score = 1477 (525.0 bits), Expect = 2.1e-151, P = 2.1e-151 Id ntities = 265/265 (100%), Positives = 265/265 (130%) 1 MHLRLISWLFIIINFMEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR 60 Query:

MHLRLISWLFIILNFMBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 60 MHLALISWLFIILNFMEYIGSQNASRGRRQRRUFNVSQGCQGGCATCSDYNGCLSCKPR

Sbjct:

Query:

Sbjct:

Spjet:

LFPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 19

LFPALERIGMKQIGVCLSSCP9GYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 19

LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNFCTKCKSGFYL 120

121 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180 HLGKCLDNCPEGLEANNHT%ECVS I VHCEVSEMNPWS PCTKKGKTCGFKRGTETRVRE I I Query:

HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEANPWSPCTKKGKTCGPKRGTETRVREII 180 121

181 QHPSAKGNLCPPTNETRKCTVQRKKCCKGERGKKGRERKRKKPNKGESKEAIPJSKSLES 240 QHPSAKGNLCPPTNETRKCTVQRKCQKGERGKKGRERKRKKPNKGESKEAI PDSKSLES Query:

QHPSAKGNLCPPTNETRKCTVQRKCGKGERGKKGRERKRKKPNKGESKZAIPDSKSLES 240 181 Sbjc::

241 SKEIPEQRENKQQQKKRKVQDKQKS 265 Query:

SKEIPEGRENKQQQKKRKVQCKQKS 265 SKEIPEGRENKQQQKKRKVQDKQKS 241 Spjct:

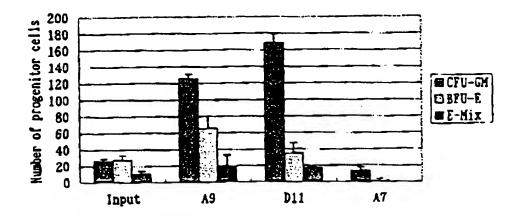


FIGURE 4

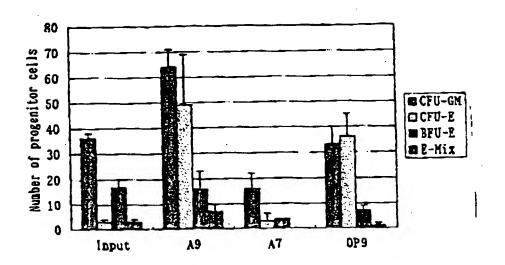


FIGURE 5

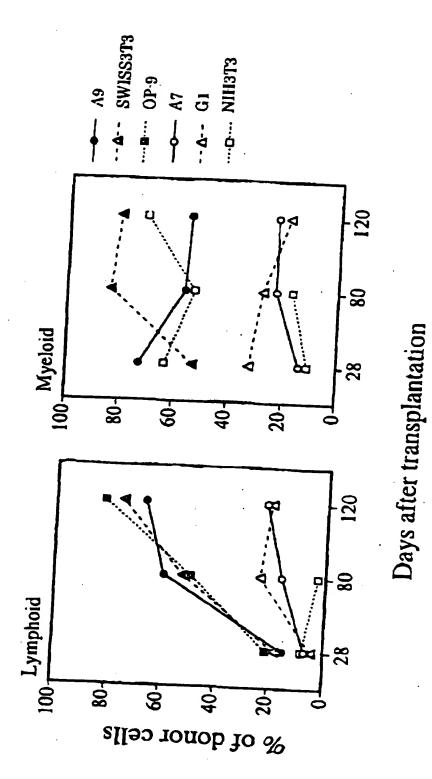
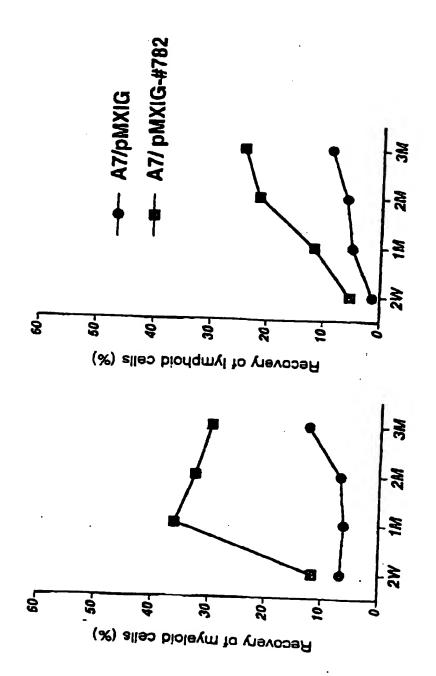


FIGURE 6



Period after transplantation

FIGURE 3